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DB Name	Query	Hit Count	Set Name
USPT,EPAB,DWPI	l8 not att	6	L9
USPT,EPAB,DWPI	muta$8 near10 (recombinase$1 near5 site$1)	16	L8
USPT,EPAB,DWPI	l6 not (lox or att)	213	L7
USPT,EPAB,DWPI	muta$8 near10 (recombin$5 adj3 site$1)	344	L6
USPT,EPAB,DWPI	l3 not lox	483	L5
USPT,EPAB,DWPI	l1 not lox	690	L4
USPT,EPAB,DWPI	l1 not att	508	L3
USPT,EPAB,DWPI	l1 near10 att	5	L2
USPT,EPAB,DWPI	muta$8 near10 (recombin$5 near5 site$1)	742	L1

L10 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2001 ACS
AN 1987:97068 CAPLUS
DN 106:97068
TI Mutational analysis of integrase arm-type binding sites of bacteriophage lambda. Integration and excision involve distinct interactions of integrase with arm-type sites
AU Bauer, Carl E.; Hesse, Steven D.; Gumport, Richard I.; Gardner, Jeffrey F.
CS Dep. Microbiol., Univ. Illinois, Urbana, IL, 61801, USA
SO J. Mol. Biol. (1986), 192(3), 513-27
CODEN: JMOBAK; ISSN: 0022-2836
DT Journal
LA English
AB Integrative recombination between specific attachment (att) regions of the bacteriophage lambda genome (attP) and the Escherichia coli genome (attB) results in a prophage flanked by the hybrid recombinant sites attL and attR. Each att site contains sequences to which proteins involved in recombination bind. Using site-directed mutagenesis, a related set of point mutations was constructed within each of the five Int arm-type binding sites located within attP, attL and attR. Footprint analyses of binding demonstrate that mutating the arm-type sites significantly disrupts the binding of Int. **Recombination** analyses of **mutant att** sites in vivo and in vitro demonstrate that only three wild-type arm-type sites within attP are required for efficient integrative recombination. Similar analyses demonstrate that efficient excision can occur with two other different sets of wild-type arm-type sites in attL and attR. Integrative and excisive recombination may involve interactions of Int with distinct and different subsets of arm-type sites.

L13 ANSWER 9 OF 11 CAPLUS COPYRIGHT 2001 ACS
AN 1997:504771 CAPLUS
DN 127:215643
TI Molecular engineering with the FRT sequence of the yeast 2.mu.m plasmid: [cir.degree.] segregant enrichment by counterselection for 2.mu.m site-specific recombination
AU Storici, Francesca; Bruschi, Carlo V.
CS Microbiology Group, ICGEB, AREA Science Park, Padriciano 99, I-34012, Trieste, Italy
SO Gene (1997), 195(2), 245-255 8/22/97
CODEN: GENED6; ISSN: 0378-1119
PB Elsevier
DT Journal
LA English
IT 195130-43-9
RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(BglII site-contg. **mutant FRT** sequence; mol. engineering with FRT sequence of yeast 2.mu.m plasmid: [cir.degree.] segregant enrichment by counterselection for 2.mu.m site-specific recombination)
IT 195130-42-8
RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(XhoI site-contg. **mutant FRT** sequence; mol. engineering with FRT sequence of yeast 2.mu.m plasmid: [cir.degree.] segregant enrichment by counterselection for 2.mu.m site-specific recombination)

L13 ANSWER 10 OF 11 CAPLUS COPYRIGHT 2001 ACS DUPLICATE 5
AN 1994:647354 CAPLUS
DN 121:247354
TI Use of Mutated FLP Recognition Target (FRT) Sites for the Exchange of Expression Cassettes at Defined Chromosomal Loci
AU Schlake, Thomas; Bode, Juergen
CS Gesellschaft fuer Biotechnologische Forschung mbH, Braunschweig-Stoeckheim, D-38124, Germany
SO Biochemistry (1994), 33(43), 12746-51
CODEN: BICHAW; ISSN: 0006-2960
DT Journal
LA English
AB Using the FLP/FRT system for site-specific recombination and the wild-type recognition site (FRT) in conjunction with certain **mutant** **FRT** sites, it becomes possible to provoke, with high yield, a double-reciprocal crossover event in cultured mammalian cells. It is demonstrated that this technol. enables a targeting of expression cassettes to appropriate chromosomal ref. sites in the recipient cell to improve the concepts of reverse genetics. The design of **mutant** **FRT** sites promoting such a process will be delineated. Our results show that the five spacer mutations tested are functional as the wild-type but differ in the extent of their cross-recombination, which has to be minimized for their simultaneous usage.
IT Mammal
(FLP/FRT system for site-specific recombination and the wild-type recognition site (**FRT**) with certain **mutant** **FRT** sites cause, with high yield, a double-reciprocal crossover event in cultured mammalian cells)
IT Recombination, genetic
(double-reciprocal; FLP/FRT system for site-specific recombination and the wild-type recognition site (**FRT**) with certain **mutant** **FRT** sites cause, with high yield, a double-reciprocal crossover event in cultured mammalian cells)
IT Recombination, genetic
(site-specific, FLP/FRT system for site-specific recombination and the wild-type recognition site (**FRT**) with certain **mutant** **FRT** sites cause, with high yield, a double-reciprocal crossover event in cultured mammalian cells)

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L9 . ANSWER 22 OF 24 CAPLUS COPYRIGHT 2001 ACS DUPLICATE 15
AN 1982:434047 CAPLUS
DN 97:34047
TI Biochemical analysis of att-defective mutants of the phage lambda site-specific recombination system
AU Ross, Wilma; Shulman, Marc; Landy, Arthur
CS Div. Biol. Med., Brown Univ., Providence, RI, 02912, USA
SO J. Mol. Biol. (1982), 156(3), 505-29
CODEN: JMOBAK; ISSN: 0022-2836
DT Journal
LA English
ST phage lambda **att mutant** sequence; DNA sequence lambda **att mutant**; recombination site specific lambda att; protein gene int binding lambda

L9 ANSWER 24 OF 24 CAPLUS COPYRIGHT 2001 ACS
AN 1971:136879 CAPLUS
DN 74:136879
TI Deletion mutants of bateriophage lambda. II. Genetic properties of att-defective mutants
AU Parkinson, John S.
CS Div. Biol., California Inst. Technol., Pasadena, Calif., USA
SO J. Mol. Biol. (1971), 56(2), 385-401
CODEN: JMOBAK
DT Journal
LA English
AB Viable, integration-defective deletion mutants of phage .lambda. were examd. with the technique of Int-promoted recombination between phages. The types of mutants found and their properties are consistent with a 3-component model of att.phi.. The results show that att.phi. contains a unique locus for integration cross-overs which is bordered on each side by recognition sequences essential for normal integration. The role of these recognition sequences in integration was studied by analyzing the pattern of Int-promoted recombination between phage contg. various types of **mutant att** sites. It was found that the integration system of .lambda. can function with a variety of defective att sites; however, no simple pattern could be deduced from these results. Evidently, the .lambda. integration system is considerably more complex than was at first believed, and very unlike systems of generalized recombination.

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